



1

SEQUENCE LISTING

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(1) GENERAL INFORMATION:

(i) APPLICANT: ANDERSON, DARRELL R.  
HANNA, NABIL  
LEONARD, JOHN E.  
NEWMAN, ROLAND A.  
REFF, MITCHELL E.  
RASTETTER, WILLIAM H.

(ii) TITLE OF INVENTION: THERAPEUTIC APPLICATION OF CHIMERIC AND  
RADIOLABELED ANTIBODIES TO HUMAN B LYMPHOCYTE RESTRICTED  
DIFFERENTIATION ANTIGEN FOR THE TREATMENT OF B CELL  
LYMPHOMA

(iii) NUMBER OF SEQUENCES: 11

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: PILLSBURY WINTHROP  
(B) STREET: 1100 New York Avenue, N.W., Ninth FL.  
(C) CITY: Washington  
(D) STATE: DC  
(E) COUNTRY: USA  
(F) ZIP: 20005

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/921,060  
(B) FILING DATE: 29-AUG-1997  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Teskin, Robin L.  
(B) REGISTRATION NUMBER: 35,030  
(C) REFERENCE/DOCKET NUMBER: 037003-0275463

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 202-861-3000  
(B) TELEFAX: 202-822-0944

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGGAGCTTGG ATCGATCCTC TATGGTT

27

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8540 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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GGAGAATGGG CGGAAGTGGG CGGAGTTAGG GGCGGGATGG GCGGAGTTAG GGGCGGGACT 180
ATGGTTGCTG ACTAATTGAG ATGCATGCTT TGCATACTTC TGCTTGCTGG GGAGCCTGGG 240
GACTTTCCAC ACCTGGTTGC TGACTAATTG AGATGCATGC TTTGCATACT TCTGCCTGCT 300
GGGGAGCCTG GGGACTTTCC ACACCCTAAC TGACACACAT TCCACAGAAT TAATTCCCCT 360
AGTTATTAAT AGTAATCAAT TACGGGGTCA TTAGTTCATA GCCCATATAT GGAGTTCCGC 420
GTTACATAAC TTACGGTAAA TGGCCCGCCT GGCTGACCGC CCAACGACCC CCGCCCATTG 480
ACGTCAATAA TGACGTATGT TCCCATAGTA ACGCCAATAG GGACTTTCCA TTGACGTCAA 540
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AGTACGCCCC CTATTGACGT CAATGACGGT AAATGGCCCG CCTGGCATTG TGCCCGAGTAC 660
ATGACCTTAT GGGACTTTCC TACTTGCGAG TACATCTACG TATTAGTCAT CGCTATTACC 720
ATGGTGATGC GGTTTTGGCA GTACATCAAT GGGCGTGGAT AGCGGTTTGA CTCACGGGGA 780
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CTCCAGGTG CACGATGTGA TGGTACCAAG GTGGAATCA AACGTACGGT GGCTGCACCA 1080
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TGCTTGCTGA ATAAGTTCTA TCCCAGAGAG GCCAAAGTAC AGTGGAAGGT GGATAACGCC 1200
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GTTTGCCCCCT CCCCCTGACC TTCCCTTGACC CTGGAAGGTG CCACTCCCAC TGTCCTTTCC 1560
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TTCCTACTTG GCAGTACATC TACGTATTAG TCATCGCTAT TACCATGGTG ATGCGGTTTT 1860
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GTAACAACTC CGCCCCATTG ACGCAAATGG CGGGTAGGCG TGTACGGTGG GAGGTCTATA 2040
TAAGCAGAGC TGGGTACGTC CTCACATTCA GTGATCAGCA CTGAACACAG ACCCGTCGAC 2100
ATGGGTTGGA GCCTCATCTT GCTCTTCTTT GTGCTGTTTG CTACGCGTGT CGCTAGCACC 2160
AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG 2220

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AACGTGAATC	ACAAGCCCAG	CAACACCAAG	GTGGACAAGA	AAGCAGAGCC	CAAATCTTGT	2460
GACAAAACCTC	ACACATGCCC	ACCGTGCCCCA	GCACCTGAAC	TCCTGGGGGG	ACCGTCAGTC	2520
TTCTCTTTCC	CCCCAAAACC	CAAGGACACC	CTCATGATCT	CCCGGACCCC	TGAGGTCACA	2580
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AACGTCTTCT	CATGCTCCGT	GATGCATGAG	GCTCTGCACA	ACCACTACAC	GCAGAAGAGC	3120
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TCTTCAGTGG	AAGGTAAACA	GAATCTGGTG	ATTATGGGTA	GGAAAACCTG	GTTCTCCATT	4140
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GCCAGTGAGT	GGCACAGCAT	TCTAGGGAGA	AATATGCTTG	TCATCACCGA	AGCCTGATTC	5100
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CTCTGATGCC	GCCGTGTTCC	GGCTGTCAGC	GCAGGGGCGC	CCGGTTCTTT	TTGTCAAGAC	5400
CGACCTGTCC	GGTGCCCTGA	ATGAAGTGA	GGACGAGGCA	GCGCGGCTAT	CGTGGCTGGC	5460
CACGACGGGC	TTTCCTTGCG	CAGCTGTGCT	CACGTTGTGC	ACTGAAGCGG	GAAGGGACTG	5520
GCTGCTATTG	GGCGAAGTGC	CGGGGCAGGA	TCTCCTGTCA	TCTCACCTTG	CTCCTGCCGA	5580
GAAAGTATCC	ATCATGGCTG	ATGCAATGCG	GCGGCTGCAT	ACGCTTGATC	CGGCTACCTG	5640
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GCTGGGTGTG	GCGGACCGCT	ATCAGGACAT	AGCGTTGGCT	ACCCGTGATA	TTGCTGAAGA	5940
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GAAATGACCG	ACCAAGCGAC	GCCCAACCTG	CCATCACGAG	ATTTTCGATTC	CACCGCCGCC	6120
TTCTATGAAA	GGTTGGGCTT	CGGAATCGTT	TTCCGGGACG	CCGGCTGGAT	GATCCTCCAG	6180
CGCGGGGATC	TCATGTGTGA	GTTCTTCGCC	CACCCCAACT	TGTTTATTGC	AGCTTATAAT	6240
GGTTACAAAT	AAAGCAATAG	CATCACAAAT	TTCACAAATA	AAGCATTTTT	TTCACTGCAT	6300
TCTAGTTGTG	GTTTGTCCAA	ACTCATCAAT	CTATCTTATC	ATGTCTGGAT	CGCGGCCGCG	6360
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CGCTCACAAAT	TCCACACAAC	ATACGAGCCG	GAAGCATAAA	GTGTAAAGCC	TGGGGTGCCT	6480
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CAGCCACTGG	TAACAGGATT	AGCAGAGCGA	GGTATGTAGG	CGGTGCTACA	GAGTTCCTGA	7200
AGTGGTGGCC	TAACACGGC	TACACTAGAA	GGACGCTATT	TGGTATCTGC	GCTCTGCTGA	7260
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AAGATCCTTT	GATCTTTTCT	ACGGGGTCTG	ACGCTCAGTG	GAACGAAAAC	TCACGTTAAG	7440
GGATTTTGGT	CATGAGATTA	TCAAAAAGGA	TCTTCACCTA	GATCCTTTTA	AATTAAAAAT	7500
GAAGTTTTAA	ATCAATCTAA	AGTATATATG	AGTAAACTTG	GTCTGACAGT	TACCAATGCT	7560
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TGATACCGCG	AGACCCACGC	TCACCGGCTC	CAGATTTATC	AGCAATAAAC	CAGCCAGCCG	7740
GAAGGGCCGA	GCGCAGAAGT	GGTCCTGCAA	CTTTATCCGC	CTCCATCCAG	TCTATTAATT	7800
GTTGCCGGGA	AGCTAGAGTA	AGTAGTTCGC	CAGTTAATAG	TTTGCGCAAC	GTTGTTGCCA	7860
TTGCTACAGG	CATCGTGGTG	TCACGCTCGT	CGTTTGATAT	GGCTTCATTC	AGCTCCGGTT	7920
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TCGGTCTCTC	GATCGTTGTC	AGAAGTAAGT	TGGCCGCAGT	GTTATCACTC	ATGGTTATGG	8040
CAGCACTGCA	TAATTCTCTT	ACTGTCATGC	CATCCGTAAG	ATGCTTTTCT	GTGACTGGTG	8100
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CGTCAATACG	GGATAATACC	GCGCCACATA	GCAGAACTTT	AAAAGTGCTC	ATCATTGGAA	8220
AACGTTCTTC	GGGGCGAAAA	CTCTCAAGGA	TCTTACCGCT	GTTGAGATCC	AGTTCGATGT	8280
AACCCACTCG	TGCACCCAAC	TGATCTTCAG	CATCTTTTAC	TTTACCAGC	GTTTCTGGGT	8340
GAGCAAAAAC	AGGAAGGCAA	AATGCCGCAA	AAAAGGGAAT	AAGGGCGACA	CGGAAATGTT	8400
GAATACTCAT	ACTCTTCCTT	TTTCAATATT	ATTGAAGCAT	TTATCAGGGT	TATTGTCTCA	8460
TGAGCGGATA	CATATTTGAA	TGTATTTAGA	AAAATAAACA	AATAGGGGTT	CCGCGCACAT	8520
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## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9209 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GACGTCGCGG	CCGCTCTAGG	CCTCCAAAAA	AGCCTCCTCA	CTACTTCTGG	AATAGCTCAG	60
AGGCCGAGGC	GGCCTCGGCC	TCTGCATAAA	TAAAAAAAAT	TAGTCAGCCA	TGCATGGGGC	120
GGAGAATGGG	CGGAAC TGGG	CGGAGTTAGG	GGCGGGATGG	GCGGAGTTAG	GGGCGGGACT	180
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GACTTTCCAC	ACCTGGTTGC	TGACTAATTG	AGATGCATGC	TTTGCATACT	TCTGCCCTGCT	300
GGGGAGCCTG	GGGACTTTCC	ACACCCTAAC	TGACACACAT	TCCACAGAAT	TAAT'TCCCCCT	360
AGTTATTAAT	AGTAATCAAT	TACGGGGTCA	TTAGTTCATA	GCCCATATAT	GGAGT'TCCGC	420
GTTACATAAC	TTACGGTAAA	TGGCCCGCCT	GGCTGACCGC	CCAACGACCC	CCGCCCATTG	480
ACGTCAATAA	TGACGTATGT	TCCCATAGTA	ACGCCAATAG	GGACTTTCCA	TTGACGTCAA	540
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TTTCCAAAGTC	TCCACCCCAT	TGACGTCAAT	GGGAGTTTGT	TTTGGCACCA	AAATCAACGG	840
GACTTTCCAA	AATGTCGTAA	CAACTCCGCC	CCATTGACGC	AAATGGGCGG	TAGGCGTGTA	900
CGGTGGGAGG	TCTATATAAG	CAGAGCTGGG	TACGTGAACC	GTCAGATCGC	CTGGAGACGC	960
CATCACAGAT	CTCTCACTAT	GGATTTTTCAG	GTGCAGATTA	TCAGCTTCCT	GCTAATCAGT	1020
GCTTCAGTCA	TAATGTCCAG	AGGACAAATT	GTTCTCTCCC	AGTCTCCAGC	AATCCTGTCT	1080
GCATCTCCAG	GGGAGAAGGT	CACAATGACT	TGCAGGGCCA	GCTCAAGTGT	AAGTTACATC	1140
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CTGGCTTCTG	GAGTCCCTGT	TCGCTTCAGT	GGCAGTGGGT	CTGGGACTTC	TTACTCTCTC	1260
ACAATCAGCA	GAGTGGAGGC	TGAAGATGCT	GCCACTTATT	ACTGCCAGCA	GTGGACTAGT	1320
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TCTGTCTTCA	TCTTCCCGCC	ATCTGATGAG	CAGTTGAAAT	CTGGAAGTGC	CTCTGTTGTG	1440
TGCCTGCTGA	ATAACTTCTA	TCCCAGAGAG	GCCAAAGTAC	AGTGGAAGGT	GGATAACGCC	1500
CTCCAATCGG	GTAAC'TCCCA	GGAGAGTGTC	ACAGAGCAGG	ACAGCAAGGA	CAGCACCTAC	1560
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TGCGAAGTCA	CCCATCAGGG	CCTGAGCTCG	CCCCTCACAA	AGAGCTTCAA	CAGGGGAGAG	1680
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GGCCGTGATA	TCTACGTATG	ATCAGCCTCG	ACTGTGCCTT	CTAGTTGCCA	GCCATCTGTT	1800
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GGCAGTACAT	CAATGGGCGT	GGATAGCGGT	TTGACTCACG	GGGATTTCCA	AGTCTCCACC	2220
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GTACAACCTGC	AGCACCTTGG	GGCTGAGCTG	GTGAAGCCTG	GGGCCTCAGT	GAAGATGTCC	2520
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CAGAAGTTCA	AAGGCAAGGC	CACATTGACT	GCAGACAAAT	CCTCCAGCAC	AGCCTACATG	2700
CAGCTCAGCA	GCCTGACATC	TGAGGACTCT	GCGGTCTATT	ACTGTGCAAG	ATCGACTTAC	2760
TACGGCGGTG	ACTGGTACTT	CAATGTCTGG	GGCGCAGGGA	CCACGGTCAC	CGTCTCTGCA	2820
GCTAGCACCA	AGGGCCCATC	GGTCTTCCCC	CTGGCACCTT	CCTCCAAGAG	CACCTCTGGG	2880
GGCACAGCGG	CCCTGGGCTG	CCTGGTCAAG	GACTACTTCC	CCGAACCGGT	GACGCTGTCTG	2940
TGGAACCTCAG	GCGCCCTGAC	CAGCGGCGTG	CACACCTTCC	CGGCTGTCTT	ACAGTCTCTCA	3000
GGACTCTACT	CCCTCAGCAG	CGTGGTGACC	GTGCCCTCCA	GCAGCTTGGG	CACCCAGACC	3060
TACATCTGCA	ACGTGAATCA	CAAGCCCAGC	AACACCAAGG	TGGACAAGAA	AGCAGAGCCC	3120

AAATCTTGTG	ACAAAACCTCA	CACATGCCCA	CCGTGCCCAG	CACCTGAACT	CCTGGGGGGA	3180
CCGTCACTCT	TCCTCTTCCC	CCCAAAACCC	AAGGACACCC	TCATGATCTC	CCGGACCCCT	3240
GAGGTCACAT	GCGTGGTGGT	GGACGTGAGC	CACGAAGACC	CTGAGGTCAA	GTTCAACTGG	3300
TACGTGGACG	GCGTGGAGGT	GCATAATGCC	AAGACAAAGC	CGCGGGAGGA	GCAGTACAAC	3360
AGCACGTACC	GTGTGGTCAG	CGTCCTCACC	GTCCTGCACC	AGGACTGGCT	GAATGGCAAG	3420
GAGTACAAGT	GCAAGGTCTC	CAACAAAGCC	CTCCCAGCCC	CCATCGAGAA	AACCATCTCC	3480
AAAGCCAAAG	GGCAGCCCCG	AGAACCACAG	GTGTACACCC	TGCCCCCATC	CCGGGATGAG	3540
CTGACCAAGA	ACCAGGTCAG	CCTGACCTGC	CTGGTCAAAG	GCTTCTATCC	CAGCGACATC	3600
GCCGTGGAGT	GGGAGAGCAA	TGGGCAGCCG	GAGAACAAC	ACAAGACCAC	GCCTCCCGTG	3660
CTGGACTCCG	ACGGCTCCTT	CTTCTCTAC	AGCAAGCTCA	CCGTGGACAA	GAGCAGGTGG	3720
CAGCAGGGGA	ACGTCTTCTC	ATGCTCCGTG	ATGCATGAGG	CTCTGCACAA	CCACTACACG	3780
CAGAAGAGCC	TCTCCCTGTC	TCCGGGTAAA	TGAGGATCCG	TTAACGGTTA	CCAACTACCT	3840
AGACTGGATT	CGTGACAACA	TGCGGCCGTG	ATATCTACGT	ATGATCAGCC	TCGACTGTGC	3900
CTTCTAGTTG	CCAGCCATCT	GTTGTTTGCC	CCTCCCCCGT	GCCTTCCTTG	ACCTTGGAAG	3960
GTGCCACTCC	CACTGTCTTT	TCCTAATAAA	ATGAGGAAAT	TGCATCGCAT	TGTCTGAGTA	4020
GGTGTCAATC	TATTCTGGGG	GGTGGGGTGG	GGCAGGACAG	CAAGGGGGAG	GATTGGGAAG	4080
ACAATAGCAG	GCATGCTGGG	GATGCGGTGG	GCTCTATGGA	ACCAGCTGGG	GCTCGACAGC	4140
GCTGGATCTC	CCGATCCCCA	GCTTTGCTTC	TCAATTTCTT	ATTTGCATAA	TGAGAAAAAA	4200
AGGAAAATTA	ATTTTAAACAC	CAATTCAGTA	GTTGATTGAG	CAAATGCGTT	GCCAAAAAGG	4260
ATGCTTTAGA	GACAGTGTTC	TCTGCACAGA	TAAGGACAAA	CATTATTTCAG	AGGGAGTACC	4320
CAGAGCTGAG	ACTCCTAAGC	CAGTGAGTGG	CACAGCAATC	TAGGGAGAAA	TATGCTTGTC	4380
ATCACCGAAG	CCTGATTCCG	TAGAGCCACA	CCTTGGTAAAG	GGCCAATCTG	CTCACACAGG	4440
ATAGAGAGGG	CAGGAGCCAG	GGCAGAGCAT	ATAAGGTGAG	GTAGGATCAG	TTGCTCCTCA	4500
CATTTGCTTC	TGACATAGTT	GTGTTGGGAG	CTTGATAGC	TTGGACAGCT	CAGGGCTGCG	4560
ATTTTCGCGCC	AAACTTGACG	GCAATCCTAG	CGTGAAGGCT	GGTAGGATTT	TATCCCCGCT	4620
GCCATCATGG	TTCGACCATT	GAAGTGCATC	GTGCGCGTGT	CCCAAAATAT	GGGGATTGGC	4680
AAGAACGGAG	ACCTACCCCTG	GCCTCCGCTC	AGGAACGAGT	TCAAGTACTT	CCAAAGAATG	4740
ACCACAACCT	CTTCAGTGGA	AGGTAAACAG	AATCTGGTGA	TTATGGGTAG	GAAAAAATGG	4800
TTCTCCATTC	CTGAGAAGAA	TCGACCTTTA	AAGGACAGAA	TTAATATAGT	TCTCAGTAGA	4860
GAAGTCAAA	AACCACCACG	AGGAGCTCAT	TTTCTTGCCA	AAAGTTTGGA	TGATGCCTTA	4920
AGACTTATTG	AACAACCGGA	ATTGGCAAGT	AAAGTAGACA	TGGTTTGATG	AGTCGGAGGC	4980
AGTTCTGTTT	ACCAGGAAGC	CATGAATCAA	CCAGGCCACC	TTAGACTCTT	TGTGACAAGG	5040
ATCATGCAGG	AATTTGAAAG	TGACACGTTT	TTCCCAGAAA	TTGATTTGGG	GAAATATAAA	5100
CTTCTCCCAG	AATACCCAGG	CGTCCTCTCT	GAGGTCCAGG	AGGAAAAAGG	CATCAAGTAT	5160
AAGTTTGAAG	TCTACGAGAA	GAAAGACTAA	CAGGAAGATG	CTTTCAAGTT	CTCTGCTCCC	5220
CTCCTAAAGC	TATGCATTTT	TATAAGACCA	TGGGACTTTT	GCTGGCTTTA	GATCAGCCTC	5280
GAAGTGTGCT	TCTAGTTGCC	AGCCATCTGT	TGTTTGCCCC	TCCCCCGTGC	CTTCCTTGAC	5340
CCTGGAAGGT	GCCACTCCCCA	CTGTCCTTTT	CTAATAAAAT	GAGGAAATTG	CATCGCATTTG	5400
TCTGAGTAGG	TGTCATTCTA	TTCTGGGGGG	TGGGGTGGGG	CAGGACAGCA	AGGGGGAGGA	5460
TTGGGAAGAC	AATAGCAGGC	ATGCTGGGGA	TGCGGTGGGC	TCTATGGAAC	CAGCTGGGGC	5520
TCGAGCTACT	AGCTTTGCTT	CTCAATTTCT	TATTTGCATA	ATGAGAAAAA	AAGGAAAATT	5580
AATTTTAACA	CCAATTCAGT	AGTTGATTGA	GCAAATGCGT	TGCCAAAAAG	GATGCTTTAG	5640
AGACAGTGTT	CTCTGCACAG	ATAAGGACAA	ACATTATTCA	GAGGGAGTAC	CCAGAGCTGA	5700
GACTCCTAAG	CCAGTGAGTG	GCACAGCATT	CTAGGGAGAA	ATATGCTTGT	CATCACCGAA	5760
GCCTGATTCC	GTAGAGCCAC	ACCTTGGTAA	GGGCCAATCT	GCTCACACAG	GATAGAGAGG	5820
GCAGGAGCCA	GGGCAGAGCA	TATAAGGTGA	GGTAGGATCA	GTTGCTCCTC	ACATTTGCTT	5880
CTGACATAGT	TGTGTTGGGA	GCTTGATCG	ATCCTCTATG	GTTGAACAAG	ATGGATTGCA	5940
CGCAGGTTCT	CCGGCCGCTT	GGGTGGAGAG	GCTATTGCGC	TATGACTGGG	CACAACAGAC	6000
AATCGGCTGC	TCTGATGCCG	CCGTGTTCCG	GCTGTCAGCG	CAGGGGCGCC	CGGTTCTTTT	6060
TGTCAAGACC	GACCTGTCCG	GTGCCCTGAA	TGAACTGCAG	GACGAGGCAG	CGCGGCTATC	6120
GTGGCTGGCC	ACGACGGGCG	TTCCTTGCGC	AGCTGTGCTC	GACGTTGTCA	CTGAAGCGGG	6180
AAGGGACTGG	CTGCTATTGG	GCGAAGTGCC	GGGGCAGGAT	CTCCTGTGAT	CTCACCTTGC	6240
TCCTGCCGAG	AAAGTATCCA	TCATGGCTGA	TGCAATGCGG	CGGCTGCATA	CGCTTGATCC	6300
GGCTACCTGC	CCATTCGACC	ACCAAGCGAA	ACATCGCATC	GAGCGAGCAC	GTAATCGGAT	6360
GGAAGCCGGT	CTTGTCGATC	AGGATGATCT	GGACGAAGAG	CATCAGGGGC	TCGCGCCAGC	6420
CGAACTGTTT	GCCAGGCTCA	AGGCGCGCAT	GCCCCAGGCG	GAGGATCTCG	TCGTGACCCA	6480
TGGCGATGCC	TGCTTGCCGA	ATATCATGGT	GGAAAAATGG	CGCTTTTCTG	GATTTCATCGA	6540
CTGTGGCCGG	CTGGGTGTGG	CGGACCGCTA	TCAGGACATA	GCGTTGGCTA	CCCGTGATAT	6600

TGCTGAAGAG	CTTGGCGGCG	AATGGGCTGA	CCGCTTCCTC	GTGCTTTACG	GTATCGCCGC	6660
TCCCGATTTCG	CAGCGCATCG	CCTTCTATCG	CCTTCTTGAC	GAGTTCTTCT	GAGCGGGACT	6720
CTGGGGTTTCG	AAATGACCGA	CCAAGCGACG	CCCAACCTGC	CATCACGAGA	TTTCGATTCC	6780
ACCGCCGCCT	TCTATGAAAG	GTTGGGCTTC	GGAATCGTTT	TCCGGGACGC	CGGCTGGATG	6840
ATCCTCCAGC	GCGGGGATCT	CATGCTGGAG	TTCTTCGCCC	ACCCCAACTT	GTTTATTGCA	6900
GCTTATAATG	GTTACAAATA	AAGCAATAGC	ATCACAAATT	TCACAAATAA	AGCATTTTTT	6960
TCACTGCATT	CTAGTTGTGG	TTTGTCCAAA	CTCATCAATC	TATCTTATCA	TGTCTGGATC	7020
GCGGCCGCGA	TCCCGTCGAG	AGCTTGGCGT	AATCATGGTC	ATAGCTGTTT	CCTGTGTGAA	7080
ATTGTTATCC	GCTCACAATT	CCACACAACA	TACGAGCCGG	AAGCATAAAG	TGTAAAGCCT	7140
GGGGTGCTTA	ATGAGTGAGC	TAACCTCACAT	TAATTGCGTT	GCGCTCACTG	CCCGCTTTCC	7200
AGTCGGGAAA	CCTGTCGTGC	CAGCTGCATT	AATGAATCGG	CCAACGCGCG	GGGAGAGGCG	7260
GTTTGCATAT	TGGGCGCTCT	TCCGCTTCCT	CGCTCACTGA	CTCGCTGCGC	TCGGTCGTTC	7320
GGCTGCGGCG	AGCGGTATCA	GCTCACTCAA	AGGCGGTAAT	ACGGTTATCC	ACAGAATCAG	7380
GGGATAACGC	AGGAAAGAAC	ATGTGAGCAA	AAGGCCAGCA	AAAGGCCAGG	AACCGTAAAA	7440
AGGCCGCGTT	GCTGGCGTTT	TTCCATAGGC	TCCGCCCCCC	TGACGAGCAT	CACAAAAATC	7500
GACGCTCAAG	TCAGAGGTGG	CGAAACCCGA	CAGGACTATA	AAGATACCAG	GCGTTTCCCC	7560
CTGGAAGCTC	CCTCGTGCGC	TCTCCTGTTT	CGACCCCTGCC	GCTTACCAGG	TACCTGTCCG	7620
CCTTTCTCCC	TTCCGGGAAGC	GTGGCGCTTT	CTCAATGCTC	ACGCTGTAGG	TATCTCAGTT	7680
CGGTGTAGGT	CGTTCGCTCC	AAGCTGGGCT	GTGTGCACGA	ACCCCCGTT	CAGCCCCGACC	7740
GCTGCGCCTT	ATCCGGTAAC	TATCGTCTTG	AGTCCAACCC	GGTAAGACAC	GACTTATCGC	7800
CACTGGCAGC	AGCCACTGGT	AACAGGATTA	GCAGAGCGAG	GTATGTAGGC	GGTGCTACAG	7860
AGTTCTTGAA	GTGGTGGCCT	AACTACGGCT	ACACTAGAAG	GACAGTATTT	GGTATCTGCG	7920
CTCTGCTGAA	GCCAGTTACC	TTCCGAAAAA	GAGTTGGTAG	CTCTTGATCC	GGCAAACAAA	7980
CCACCGCTGG	TAGCGGTGGT	TTTTTTGTTT	GCAAGCAGCA	GATTACGCGC	AGAAAAAAG	8040
GATCTCAAGA	AGATCCTTTG	ATCTTTTCTA	CGGGGTCTGA	CGCTCAGTGG	AACGAAAACT	8100
CACGTTAAGG	GATTTTGGTC	ATGAGATTAT	CAAAAAGGAT	CTTCACCTAG	ATCCTTTTAA	8160
ATTAAAAATG	AAGTTTTTAA	TCAATCTAAA	GTATATATGA	GTAACCTTGG	TCTGACAGTT	8220
ACCAATGCTT	AATCAGTGAG	GCACCTATCT	CAGCGATCTG	TCTATTTCTG	TCATCCATAG	8280
TTGCCTGACT	CCCCGTCGTG	TAGATAACTA	CGATACGGGA	GGGCTTACCA	TCTGGCCCCA	8340
GTGCTGCAAT	GATACCGCGA	GACCCACGCT	CACCGGCTCC	AGATTTATCA	GCAATAAACC	8400
AGCCAGCCGG	AAGGGCCGAG	CGCAGAAGTG	GTCCTGCAAC	TTTATCCGCC	TCCATCCAGT	8460
CTATTAATTG	TTGCCGGGAA	GCTAGAGTAA	GTAGTTCGCC	AGTTAATAGT	TTGCGCAACG	8520
TTGTTGCCAT	TGCTACAGGC	ATCGTGGTGT	CACGCTCGTC	GTTTGGTATG	GCTTCATTCA	8580
GCTCCGGTTC	CCAACGATCA	AGGCGAGTTA	CATGATCCCC	CATGTTGTGC	AAAAAAGCGG	8640
TTAGCTCCTT	CGGTCTCTCC	ATCGTTGTCA	GAAGTAAGTT	GGCCGCAAGT	TTATCACTCA	8700
TGGTTATGGC	AGCACTGCAT	AATTCTCTTA	CTGTCAATGCC	ATCCGTAAGA	TGCTTTTCTG	8760
TGACTGGTGA	GTAATCAACC	AAGTCATTCT	GAGAATAGTG	TATGCGGCGA	CCGAGTTGCT	8820
CTTGCCCGGC	GTCAATACCG	GATAATACCG	CGCCACATAG	CAGAACTTTA	AAAGTGCTCA	8880
TCATTGGAAA	ACGTTCTTCG	GGGCGAAAAA	TCTCAAGGAT	CTTACCGCTG	TTGAGATCCA	8940
GTTTCGATGTA	ACCCACTCGT	GCACCCAACT	GATCTTCAGC	ATCTTTTACT	TTCACCAGCG	9000
TTTCTGGGTG	AGCAAAAACA	GGAAGGCAAA	ATGCCGCAAA	AAAGGGAATA	AGGGCGACAC	9060
GGAAATGTTG	AATACTCATA	CTCTTCCTTT	TTCAATATTA	TTGAAGCATT	TATCAGGGTT	9120
ATTGTCTCAT	GAGCGGATAC	ATATTTGAAT	GTATTTAGAA	AAATAAACAA	ATAGGGGTTT	9180
CGCGCACATT	TCCCCGAAAA	GTGCCACCT				9209

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATCACAGATC TCTCACCATG GATTTTCAGG TGCAGATTAT CAGCTTC

47

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer"

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TGCAGCATCC GTACGTTTGA TTTCCAGCTT

30

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..384

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATG GAT TTT CAG GTG CAG ATT ATC AGC TTC CTG CTA ATC AGT GCT TCA	48
Met Asp Phe Gln Val Gln Ile Ile Ser Phe Leu Leu Ile Ser Ala Ser	
1 5 10 15	
GTC ATA ATG TCC AGA GGG CAA ATT GTT CTC TCC CAG TCT CCA GCA ATC	96
Val Ile Met Ser Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile	
20 25 30	
CTG TCT GCA TCT CCA GGG GAG AAG GTC ACA ATG ACT TGC AGG GCC AGC	144
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser	
35 40 45	
TCA AGT GTA AGT TAC ATC CAC TGG TTC CAG CAG AAG CCA GGA TCC TCC	192
Ser Ser Val Ser Tyr Ile His Trp Phe Gln Gln Lys Pro Gly Ser Ser	
50 55 60	



CCC AAA CCC TGG ATT TAT GCC ACA TCC AAC CTG GCT TCT GGA GTC CCT	240
Pro Lys Pro Trp Ile Tyr Ala Thr Ser Asn Leu Ala Ser Gly Val Pro	
65 70 75 80	
GTT CGC TTC AGT GGC AGT GGG TCT GGG ACT TCT TAC TCT CTC ACA ATC	288
Val Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile	
85 90 95	
AGC AGA GTG GAG GCT GAA GAT GCT GCC ACT TAT TAC TGC CAG CAG TGG	336
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp	
100 105 110	
ACT AGT AAC CCA CCC ACG TTC GGA GGG GGG ACC AAG CTG GAA ATC AAA	384
Thr Ser Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys	
115 120 125	

## (2) INFORMATION FOR SEQ ID NO:7:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Asp Phe Gln Val Gln Ile Ile Ser Phe Leu Leu Ile Ser Ala Ser	
1 5 10 15	
Val Ile Met Ser Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile	
20 25 30	
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser	
35 40 45	
Ser Ser Val Ser Tyr Ile His Trp Phe Gln Gln Lys Pro Gly Ser Ser	
50 55 60	
Pro Lys Pro Trp Ile Tyr Ala Thr Ser Asn Leu Ala Ser Gly Val Pro	
65 70 75 80	
Val Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile	
85 90 95	
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp	
100 105 110	
Thr Ser Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys	
115 120 125	

## (2) INFORMATION FOR SEQ ID NO:8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCGGCTCCCA CGCGTGTCTT GTCCCAG

27

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "primer"

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGSTGTTGTG CTAGCTGMRG AGACRGTGA

29

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 420 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 1..420

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATG GGT TGG AGC CTC ATC TTG CTC TTC CTT GTC GCT GTT GCT ACG CGT  
Met Gly Trp Ser Leu Ile Leu Leu Phe Leu Val Ala Val Ala Thr Arg  
1 5 10 15

48

GTC CTG TCC CAG GTA CAA CTG CAG CAG CCT GGG GCT GAG CTG GTG AAG  
Val Leu Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys  
20 25 30

96

CCT GGG GCC TCA GTG AAG ATG TCC TGC AAG GCT TCT GGC TAC ACA TTT	144
Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe	
35 40 45	
ACC AGT TAC AAT ATG CAC TGG GTA AAA CAG ACA CCT GGT CGG GGC CTG	192
Thr Ser Tyr Asn Met His Trp Val Lys Gln Thr Pro Gly Arg Gly Leu	
50 55 60	
GAA TGG ATT GGA GCT ATT TAT CCC GGA AAT GGT GAT ACT TCC TAC AAT	240
Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn	
65 70 75 80	
CAG AAG TTC AAA GGC AAG GCC ACA TTG ACT GCA GAC AAA TCC TCC AGC	288
Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser	
85 90 95	
ACA GCC TAC ATG CAG CTC AGC AGC CTG ACA TCT GAG GAC TCT GCG GTC	336
Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val	
100 105 110	
TAT TAC TGT GCA AGA TCG ACT TAC TAC GGC GGT GAC TGG TAC TTC AAT	384
Tyr Tyr Cys Ala Arg Ser Thr Tyr Tyr Gly Gly Asp Trp Tyr Phe Asn	
115 120 125	
GTC TGG GGC GCA GGG ACC ACG GTC ACC GTC TCT GCA	420
Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ala	
130 135 140	

## (2) INFORMATION FOR SEQ ID NO:11:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Gly Trp Ser Leu Ile Leu Leu Phe Leu Val Ala Val Ala Thr Arg	
1 5 10 15	
Val Leu Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys	
20 25 30	
Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe	
35 40 45	
Thr Ser Tyr Asn Met His Trp Val Lys Gln Thr Pro Gly Arg Gly Leu	
50 55 60	
Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn	
65 70 75 80	
Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser	
85 90 95	

Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val  
100 105 110

Tyr Tyr Cys Ala Arg Ser Thr Tyr Tyr Gly Gly Asp Trp Tyr Phe Asn  
115 120 125

Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ala  
130 135 140

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